

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 18, 2001, 15:34:08 ; Search time 78.57 Seconds
(without alignments)
777,968 Million cell updates/sec

Title: US-09-653-755A-6

Perfect score: 2487
Sequence: 1 EVQLOOSGEIYKPGASVMI.....YIAKTIKSRSPKSGHHHHHH 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_16:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.rodent:*
13: sp.unclassified:*
14: sp.vertebrate:*
15: sp.virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1426	57.3	437	11 09R1A4	09R1A4 mus musculu
2	547	22.0	416	4 09NPP6	09NPP6 homo sapien
3	480.5	19.3	117	11 09QXF0	09QXF0 mus musculu
4	477	19.2	384	4 09UP60	09UP60 homo sapien
5	458.5	18.4	117	11 09QXE9	09QXE9 mus musculu
6	414	16.6	109	11 09UL75	09UL75 mus musculu
7	401	16.1	118	11 09ZIC4	09ZIC4 mus musculu
8	385	15.5	114	11 09UL81	09UL81 mus musculu
9	379	15.2	110	11 09UL77	09UL77 mus musculu
10	372.5	15.0	684	13 090544	090544 ginglymosto
11	371.5	14.9	150	4 09Y298	09Y298 homo sapien
12	369.5	14.9	157	4 09S978	09S978 homo sapien
13	366.5	14.7	119	5 09GY22	09GY22 schistosoma
14	364	14.6	124	4 09UL92	09UL92 homo sapien
15	358.5	14.4	109	11 09UL85	09UL85 mus musculu
16	356	14.3	110	11 09UL83	09UL83 mus musculu
17	353.5	14.2	119	4 09UL94	09UL94 homo sapien
18	349.5	14.1	117	11 09ZIC6	09ZIC6 mus musculu
19	348.5	14.0	125	4 09UL95	09UL95 homo sapien

20	328	13.2	116	4 09UL89	09UL89 homo sapien
21	328	13.2	147	4 09Y509	09Y509 homo sapien
22	294.5	11.8	119	4 09UL73	09UL73 homo sapien
23	294.5	11.8	298	11 09QYF0	09QYF0 mus musculu
24	284.5	11.4	113	4 09UL90	09UL90 homo sapien
25	284	11.4	118	4 09UL72	09UL72 homo sapien
26	283	11.4	112	4 09HCC1	09HCC1 homo sapien
27	279	11.2	122	4 09UL84	09UL84 homo sapien
28	278	11.2	118	4 09UL91	09UL91 homo sapien
29	277.5	11.2	116	4 09UL93	09UL93 homo sapien
30	270.5	10.9	131	4 09UL88	09UL88 homo sapien
31	268.5	10.8	121	4 09UL71	09UL71 homo sapien
32	266	10.7	150	4 09S973	09S973 homo sapien
33	261.5	10.5	102	11 09UL79	09UL79 mus musculu
34	251	10.1	124	6 09N0W6	09N0W6 oryctolagus
35	249	10.0	124	6 09N0W4	09N0W4 oryctolagus
36	243	9.8	122	4 09UL75	09UL75 homo sapien
37	237.5	9.5	104	4 09UL87	09UL87 homo sapien
38	234.5	9.4	121	4 09UL96	09UL96 homo sapien
39	222.5	8.9	112	4 09UGP3	09UGP3 homo sapien
40	212	8.5	95	4 09ULB6	09ULB6 homo sapien
41	189.5	7.6	88	4 075737	075737 homo sapien
42	187	7.5	268	13 090524	090524 ginglymosto
43	182.5	7.3	75	4 075743	075743 homo sapien
44	179	7.2	267	13 090529	090529 ginglymosto
45	176.5	7.1	77	4 075741	075741 homo sapien

ALIGNMENTS

RESULT	1	PREDIMINARY	PRT	437 AA.
09R1A4	AC	09R1A4		
ID	09R1A4			
AC	09R1A4			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Wildie K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;			
RT	"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a			
RT	single chain antibody (scFv).";			
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF152372; AAD40243.1; -			
DR	HSSP; P01842; 7FAB.			
DR	InterPro; IPR003600; -			
DR	InterPro; IPR003600; -			
DR	Pfam; PF00047; 1g; 4.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			
DR	SMART; SM00410; IG_Like; 1.			
FT	NON_TER			
FT	NON_TER			
SO	SEQUENCE			

Query Match 57.3%; Score 1426; DB 11; Length 437;
Best Local Similarity 60.0%; Pred. No. 2.3e-103;
Matches 275; Conservative 63; Mismatches 94; Indels 26; Gaps 8;

QY	2	VOLQOSGEIYKPGASVMI	SCRTSAVFTENTVMVWQSHSELEMT	-----GGINPYG	56
DB	1	VOLDGGGLVKGSLKLS	CAASGFTFSYAMSVRQTPKRLWASFSGGI	-IYT	59
QY	57	GSISPKFKGKATLV	VDKSSSTAYMELSLTSED	SAVYCCARRAGAYFDWGGTTLTV	116
DB	60	DSV-----KGRFTYKXDR	NIILSIQMSLSRSEDTAM	YCAR---GDYSATWGTGTLTV	111

Oy	117	SAKTTPEPVYPLAPCCGDTTSSVYLGLVNGIFPESVTVMNNSSLSSVHTPALLO	176
Dd	112	SAAKTTPEPVYELARBSAQTNSMTLGLVKCYFEPETVTVNMSSLSIGVTFPAVLQ	171
Oy	177	SGLYTMSSSVTPWSPSOTVTCVAHPASSTTYDNLKEPSGPISITINPCPKCECHKC	236
Dd	172	SGLYTLSSSVTPWSPSEPTVCNAHNASSTKVKKTIYP-----RDC-GCKPC-IC	222
Oy	237	PAPNIEGGSVFLFPNNIDVLMISLTPTVTCVVNVSEDPPDYOLSWPFVNNEVHTAQT	296
Dd	223	TYPEVS---SVFIFFPKPRVDLTLTLPKATCVYVDISKDEPVQSWFYDDVEVHTAQT	279
Oy	297	QTHREDYNSTIRVSTLPIQHODMWSGKEFKCKVNNKDLSPSIERTISKILGVRAPOYV	356
Dd	280	QREGFENFTFSVSELPIMHODWLNGKEFKFCVNSAAPAPAEKTISTSKTGGRAPAOYV	339
Oy	357	ILPRAEQLSRKDYSITCLVAFNPEDISEVENTSNHTEENTKYMDTAPLYDSOSYTIYSK	416
Dd	340	TIIPPEQAAKRVSLTCTITDPFDPDITVEQMOMQAPANKNTOPIMTDYSITYVSK	399
Oy	417	LNMKTSKWEKTDSTFSCNAVHEGLKNYYLKTKTISRSPGX	454
Dd	400	LNVQKSMEAGNTFTGCSSLHEGLHNHTEKKNLSHSXG	437
<hr/>			
RESULT	2		
ID	Q9NPP6	PRELIMINARY;	PRT; 416 AA.
Q9NPP6			
AC	Q9NPP6;		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	IMMUNOGLOBULIN HEAVY CHAIN VARIANT (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Pluvinet R., Estivill X., Escarceller M., Sumoy L.		
RA	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Aufrey C., Ansoerge W., Ballabio A., Estivill X., Gibson K.,		
RA	Lehrach H., Poustka A., Lundberg J.		
RT	"The European IMAGE consortium for integrated Molecular analysis of		
RT	human gene transcripts."		
RT	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AL389978; CAB97534.1; -.		
DR	InterPro; IPR003006; -.		
DR	InterPro; IPR003596; -.		
DR	Pfam; PF00047; Ig; 4.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.		
DR	SMART; SM00406; Igv; 1.		
FT	NON_TER		
EQ	SEQUENCE 416 AA; 44786 MW; 8C4108BBAB4687 CRC64;		

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Query Match      22.0%: Score 547; DB 4; Length 416;
Best Local Similarity 33.3%; Pred. No. 8, 5e-35;
Matches 144; Conservative 76; Mismatches 164; Indels 48; Gaps 19.

QY    42 GESLEWIGGINYYGSGSIFSPKKKAKITLVTKSSSTAYMELRSLSEDSAYYYCARRAG 101
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     2 GKGLEWVRISSGDPTVDYADSVKGRFTVSRDTANKNSLQMSLRVEDTAYYYCAR--- 58

QY    102 AYY-EDVMGGCGTLTVSSAKTTPPSVYPLAPCCGPT--GSSVTGLCLVKGYF-ESVIV 157
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db     59 TTYGDMDVGCGTTVVSSASPTSPRYFPFLST---DSTDODGNMVVAACVLQGFEPPLEPV 115

QY    158 TWNMSGSLSSSVHTFPALAQSG--LVTMSSSYVPVPSWTW-SQTIVCSVAH----PASSTIV 211
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Db	116	TWSEGGQNTAANPPPSQDASGDLVYTTSSQTLTPATQCGPDGKSVTCHVKNHTYTPSQDVTV	175
Oy	212	DKKLEPSSPISITINCPPECKCHKCAPMLEGSPSVFIPFPINKDVLMSIPKVCYVY	271
Db	176	P-----CPVPPPPC-CH-----PRISLRHPALEDLGDS-EANLTCTLT	213
Oy	272	DVSEDDPDVQISMFPANNVEVHTAQTOTHRREDYNSTRVYSTLPICHOQMMSGKEFKCKVY	311
Db	214	GL-RASAGATFTWTPSSGK--SANGGPRPERDLCGCVSYSVLPGCAQPNNHGTFCTLA	270
Oy	332	NKDLPSPLERTISKIGLVARQVYILPPPAQLSKD-VSLTCLVGGNPGDISWETS	390
Db	271	HELTPTPLANTTK-SGNTFREVEHLPPSEELANLELVTLTCLARGSPKDVLRWLO	329
Oy	391	NGH--TEENKYRTAVLD-SDG--SVFIYSKINMTKSKMEKTDVFCSCANVRHEGLKNYULK	445
Db	330	GSQELPREVYLTWASRQEFSGCTTFPAVYILRVAAEDMKKDDTFSCMVGHEALPLATFQ	389
Oy	446	KTISRSPGKGGH 457	
Db	390	KTIDRLAGKPTH 401	
RESULT	3		
O9QXF0	1D	PRELIMINARY:	PRT: 117 AA.
AC	O9QXF0:		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Clemens A., Rademakers A., Specht C., Koelsch E.;		
RL	Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.		
DR	EMBL, AJ225171, CAB65236.1; --		
DR	InterPro; IPR003006; --		
DR	InterPro; IPR003596; --		
DR	Pfam; PF00047; 1g; 1.		
DR	SMART; SMO0406; IGV; 1.		
FT	NON_TER 1		
FT	NON_TER 117		
FT	NON_TER 117		
Q0	SEQUENCE 117 AA; 13060 MW; DB16AD0858AA7E4C CRC64;		

Query Match	19.3%	Score 480.5	DB 11	Length 117
Best Local Similarity	78.8%	Pred. No. 2.7e-30		
Matches 93	Conservative 9	Mismatches 15	Indels 1	Gaps 1
Qy	1	EVQLQQSGPELVKPGASVYMSICRTSAVYFTENTVHWVKOSHSELEMTIGINPPYGGSLF	60	
Dd	1	EVQLQQSGPELVKPGASVYMSICKAGSYFTFDYMMKVMKQSHGSKLEWIGIDINPNNGTSTY	60	
Qy	61	SPKRGKATITLVYDKSSSTAIYMELRSLTSEDSAVYICARRAGAIYEDYWGQGTTLTYSS	118	
Dd	61	NQKRGKATITLVYDKSSSTAIYMQLNLSLTSEDSAVYICARDKD-YFEDYWGQGTTLTYSS	117	
RESULT	4			
Q9UP60				
ID	Q9UP60	PRELIMINARY	PRT	384 AA.
AC	Q9UP60			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update).		
DE	SNC73 PROTEIN.			
GN	SNC73			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RT "Humanized porcine VCM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN
DR EMBL: U78801; AAD00293.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EBC559D31E4FC CRC64;

Query Match 16.1%; Score 401; DB 11; Length 118;
Best Local Similarity 65.3%; Pred. No. 4.3e-24;
Matches 77; Conservative 12; Mismatches 29; Indels 0; Gaps 0;

QY 1 EVOLQSGELVPGASVMISCTSAVTETENTVHWKOSHGSELMIGINPYGSGIP 60
DB 1 QVQVQSGALPMAVSKKASGYNFNSYMWKORPGGLEMGITAYPGDDTSY 60
DB 61 SPFKKATLTVDKSSSTAYMELRSLTSEDSAVYCARAGAYFPYWGQTTLVSS 118
DB 61 TQFKRKATLTADKSSSTAYMOLSLASEDSAVYCARRTVGSGYFPYWGQTTLVSS 118

RESULT 8
Q9JLB1 PRELIMINARY; PRT; 114 AA.

ID Q9JLB1
AC Q9JLB1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA Malikel S., Lao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206025; AAF69323.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;

Query Match 15.5%; Score 385; DB 11; Length 114;
Best Local Similarity 66.7%; Pred. No. 7.3e-23;
Matches 76; Conservative 11; Mismatches 23; Indels 4; Gaps 1;

QY 9 PELVKGASVMISCTSAVTETENTVHWKOSHGSELMIGINPYGSGIPFKRGA 68
DB 1 POLVGRGASVTKSKKASGYSFTSYMWKORPGGLEMGITAYPGDDTSY 60
QY 63 TLTVDKSSSTAYMELRSLTSEDSAVYCARAGAYFPYWGQTTLVSS 118

DB 61 TLTVDKSSSTAYMOLSLSPSEDSAVYCARSNYGGSLYFPYWGQTTLVSS 114

RESULT 9

ID Q9JL77 PRELIMINARY; PRT; 110 AA.

AC Q9JL77;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2;
RA Malikel S., Lao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF206025; AAF69327.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; 1g; 1.
DR SMART: SM00406; 1g; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12138 MW; 2EDEB81F5B62C9AF CRC64;

Query Match 15.2%; Score 379; DB 11; Length 110;
Best Local Similarity 65.7%; Pred. No. 2.1e-22;
Matches 71; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 11 LVKPGASVMISCTSAVTETENTVHWKOSHGSELMIGINPYGSGIPSPFKRATL 70
DB 3 LVKPGASVTKSKKASGYSFTSYMWKORPGGLEMGITAYPGDDTSY 62
QY 71 TVDKSSSTAYMELRSLTSEDSAVYCARAGAYFPYWGQTTLVSS 118
DB 63 TVDTSSSTAYVLDLSTSEDSAVYCARORNYAMDYWGQTSYVSS 110

RESULT 10

Q90544 PRELIMINARY; PRT; 684 AA.

ID Q90544
AC Q90544;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE NOVEL ANTIGEN RECEPTOR PRECURSOR.
OS Gingivostoma citrarium (Nurse shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Orectolobiformes;
OX Ginglymostomatidae; Ginglymostoma.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RX MEDLINE=95183140; PubMed=7877689;
RA Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks."
RL Nature 374:168-173(1995).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: U18701; AAB48195.1; -
DR HSPF; P01857; 1fc1.
DR InterPro: IPR003006; -
DR InterPro: IPR003597; -

DR Pfam; PF00047; Ig; 6.
DR SMART; PS00290; IG_MHC; UNKNOWN_3.
DR SMART; SM00407; IG1; 1.
KW Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 684 NOVEL ANTIGEN RECEPTOR.
SQ SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDA6D6D CRC64;

Query Match 15.0%; Score 372.5; DB 13; Length 684;
Best Local Similarity 23.6%; Pred. No. 6.6e-21;
Matches 130; Conservative 88; Mismatches 205; Indels 129; Gaps 23;

QY 2 VOLOQSGPELVKPGASVMISCRSATYFTEN-TYHM-----VQSGSGE- 43
DB 145 VSLHSAITEBORANRFVOLVCLISGY-YPENIAVSMOKNKTITSGFATTSPTVSSND 203
QY 44 -----SL-----EWIGGINPYGSGIFPKFKATLTVD-----KSSSTAYMELRSLTSED 90
DB 204 SCASLAKVPIQEW-----SRGSVYGCQVSHSATSSNOKREIRSTEINAVLRDPYEE 256
QY 91 -----SAVYIC-----ARRAGAYF-----DY 107
DB 257 IMIDKSATLICEVLSTVSAGVYVSMVNGKVRNEGVOEMPTKMGNOYLFTISRLTSVVE 316
QY 108 MGOSTLTIVSS-----AKTTPSYVPLAPGCGD-TTGSSTVLTGCLVKG 149
DB 317 MOSGEVETCSKKQDOSTPVYKTRKARVEPTKPLRLLPSPREIOSTTSATLTCLIRG 376
QY 150 YFPESVTVTNNSG--SLSSSVHPFALLQSL-YTMSSSVTPVSPSTWPS-QTVTCVAHP 205
DB 377 FYDPKVSVMQKDVSVSANTNFTALQDLTFSTSLNLTAVEKMSGAKYCTASHP 436
QY 206 ASSTVDKLEKPSGPISITINCPCKECHKCPADNLEGGSVETFPNIKDVIMISLTPK 265
DB 437 PSOSTVKRVIR-----NOKVDCROT-----DISVSLKPPFEET-WTQQTAT 477
QY 266 VTCVYVVDSEDDPDVOISWPFANNVEVHTAQOTHRREDYNSIRVSVTLPIQHOMWSGKE 325
DB 478 IVCEI--VYSDLENIKVFQWQVNGERRKGVETQNPWMSGSKSTVSKIKVWASMDSGTE 535
QY 326 FKCVYNNKDLPSPIERTISKIK-GLVRAPQVYILPPAEOL-SKDOVSLTCLVVGFPNGD 383
DB 536 YVCLVEDESELTPTPKASIRKANSQMPKRYLLHPSTDEIDTENSATLMCLANFHPAE 595
QY 384 ISVEWTSNGH-TEENYKDTAPVLDSDGSFYTSKLNKTSKWEKTDSESCNVRHEGLKNY 442
DB 596 IYVGMMANDTLDSGYRQYVDSEKSGSSPFYDRLRLTALEMNSDITYSCLVGHPSLNRD 655
QY 443 YLKTISRSPCK 454
DB 656 LIRST-NKSNCK 666

RESULT 11
Q9Y298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE ICG VH PROTEIN PRECURSOR (FRAGMENT).
GN ICG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with an

RT Inhibitor."
RL BLOD 92:496-506(1998).
CC -1- SIMILARITY: TO IMMNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ224083; CAA11829.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 14.9%; Score 371.5; DB 4; Length 150;
Best Local Similarity 56.6%; Pred. No. 1.2e-21;
Matches 73; Conservative 18; Mismatches 37; Indels 1; Gaps 1;

QY 1 EVOLOQSGPELVKPGASVMISCRSATYFTENTYHWMKOSHGESLEWIGINPYGSGIF 60
DB 20 QVOLVQSGAEYKPKGASVSKVSGYTLTLPVHMWQAGKGLWVGSEDPSSGSIT 79
QY 61 SPKFKATLTVDRSSSTAYMELRSLTSEDSAVYVCARAGAYFEDYWGOSTLTIVSAK 120
DB 80 AREFGSAYTMADSTDIAYMELSLSDPTAYYCA-VPPDPAFDIMGOSTMTVSSAS 138
QY 121 TTPPSVYPL 129
DB 139 TKGPSVEPL 147

RESULT 12
Q9Y298 PRELIMINARY; PRT; 157 AA.
AC Q9Y298;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VH1 PROTEIN PRECURSOR (FRAGMENT).
GN VH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RA Jox A., Zander T., Kuipers R., Irsch J., Kanzier H., Kornacker M.,
RA Bonlen H., Diehl V., Wolf J.;
RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT patient with mixed cellularity Hodgkin's disease is associated with
RT somatic mutations within the untranslated regions of rearranged and
RT class switch recombined Ig genes";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases
CC -1- SIMILARITY: TO IMMNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AJ005570; CAA06599.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003596; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17304 MW; 86986EDDA84D8B5 CRC64;

Query Match 14.9%; Score 369.5; DB 4; Length 157;
Best Local Similarity 51.9%; Pred. No. 1.8e-21;
Matches 70; Conservative 25; Mismatches 35; Indels 5; Gaps 2;

QY 1 EVOLOQSGPELVKPGASVMISCRSATYFTENTYHWMKOSHGESLEWIGINPYGSGIF 60

Db 20 QVQLVSGAIEIKPGASVYVHCTSGYVFTSYIHVVRPGCGLEWGGIGPGVSTMC 79
QY 61 SPFKGKATLVYDKSSSTAYMELRSLTSDSAVYCAR----RAGAYDYDMGCGTTLV 116
Db 80 AEFKQGLTMTKRTSTTYVLMELSLRLFEEDTAVYFCGRGRWSGNV-GHMGQGPVTV 138
QY 117 SSKATTPPSVYPLAP 131
Db 139 SSSSTKGPSPVPLAP 153

RESULT 13

Q9GY22 PRELIMINARY; PRT; 119 AA.
AC Q9GY22;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE MONOCLONAL ANTI-IDIOYPTIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the heavy chain variable region gene of monoclonal anti-idiotypic antibody NP30 of Schistosoma japonicum."
RT Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF282622; AAG01452.1; -
RL NON_TER 1
FT NON_TER 1
SQ SEQUENCE 119 AA; 13567 MW; BA893873FD5FA6AB CRC64;

Query Match 14.7%; Score 366.5; DB 5; Length 119;
Best Local Similarity 60.5%; Pred. No. 2.2e-21;
Matches 72; Conservative 17; Mismatches 29; Indels 1; Gaps 1;

QY 1 EVQLQSGPELVKPGASVMIQRTSAVYFTEENTVHWVKQSHGESLEWIGINPYGGSIF 60
Db 1 QVQLVSGAIEIKPGASVYVHCTSGYVFTSYIHVVRPGCGLEWGGIGPGVSTMC 79
QY 61 SPFKGKATLVYDKSSSTAYMELRSLTSDSAVYCARAGAY-FDYWGCGTTLTVSS 118
Db 61 NQKFKDRVTMTDKSFSTAYMDLRSLRSADSAVYCARYYDDHYCLDWGCGTTVVSS 119

RESULT 14

Q9UL92 PRELIMINARY; PRT; 124 AA.

AC Q9UL92;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.
DR EMBL: AF035022; AAD56258.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

Query Match 14.6%; Score 364; DB 4; Length 124;
Best Local Similarity 56.3%; Pred. No. 3.6e-21;
Matches 71; Conservative 19; Mismatches 26; Indels 10; Gaps 2;

QY 1 EVQLQSGPELVKPGASVMIQRTSAVYFTEENTVHWVKQSHGESLEWIGINPYGGSIF 60
Db 1 QVQLVSGAIEIKPGASVYVHCTSGYVFTSYIHVVRPGCGLEWGGIGPGVSTMC 79
QY 61 SPFKGKATLVYDKSSSTAYMELRSLTSDSAVYCARAGAY-----FDYWGCGT 112
Db 61 AAKFGQRTVMTDTSYVYLMELSLRSEDFAVYCAR--GLYVYVPAFSDYWGCGT 118
QY 113 TLTVSS 118
Db 119 LVTYSS 124

RESULT 15

Q9JL85 PRELIMINARY; PRT; 109 AA.

AC Q9JL85;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BALE/C;
RA Maikell S., Iiao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RT Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF206021; AAF69319.1; -
DR InterPro: IPR003006; -
DR InterPro: IPR003596; -
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 109 AA; 11944 MW; DFE615FECED4EDE CRC64;

Query Match 14.4%; Score 358.5; DB 11; Length 109;
Best Local Similarity 63.3%; Pred. No. 8.1e-21;
Matches 69; Conservative 13; Mismatches 26; Indels 1; Gaps 1;

QY 10 ELVKGASVMIQRTSAVYFTEENTVHWVKQSHGESLEWIGINPYGGSIFSPKFKGAT 69
Db 2 ELVKGASVMIQRTSAVYFTEENTVHWVKQSHGESLEWIGINPYGGSIFSPKFKGAT 69
QY 70 LTVKSSSTAYMELRSLTSDSAVYCARAGAYFDYWGCGTTLTVSS 118
Db 62 LTVKSSSTAYMELRSLTSDSAVYCARAGAYFDYWGCGTTLTVSS 118

Search completed: June 19, 2001, 15:34:08
Job time: 231 sec

